

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Daggett, Lorrie P.
Ellis, Steven B.
Liaw, Chen W.
Lu, Chin-Chun
- (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, DNA ENCODING SAME AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
(B) STREET: 444 South Flower Street, Suite 2000
(C) CITY: Los Angeles
(D) STATE: CA
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2921
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 20-APR-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/052,449
(B) FILING DATE: 20-APR-1993
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Reiter, Stephen E.
(B) REGISTRATION NUMBER: 31,192
(C) REFERENCE/DOCKET NUMBER: P41 9424
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619-546-4737
(B) TELEFAX: 619-546-9392

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 262..3078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC CGGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1 5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15 20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30 35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45 50	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60 65	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75 80	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95 100	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110 115	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125 130	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140 145	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
155 160	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	185
175 180	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	200
190 195	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	215
205 210	

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ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963
Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	
220						225					230					
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	GTG	TGG	CTG	GTC	GGC	1011
Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	
235					240					245					250	
GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	GCC	CCA	GAC	GGC	ATC	1059
Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	
				255					260					265		
CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	TCG	GCC	CAC	ATC	AGC	1107
Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	
			270					275					280			
GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	GAG	CTC	CTC	GAG	AAG	1155
Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	
		285					290					295				
GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	GGC	AAC	ACC	AAC	ATC	1203
Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	
300						305					310					
TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	1251
Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	
315					320					325					330	
GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	1299
Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	
				335					340					345		
AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	1347
Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	
			350					355					360			
CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	1395
Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	
		365					370					375				
ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	1443
Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	
380						385					390					
TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	1491
Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	
395					400					405				410		
GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	1539
Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	
				415					420					425		
AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	1587
Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	
			430				435						440			
TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	1635
Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	
		445					450					455				
TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	1683
Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	
		460				465					470					
GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731
Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	
475					480					485					490	

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AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC	1779
Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu	
495 500 505	
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG	1827
Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu	
510 515 520	
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG	1875
Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu	
525 530 535	
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC	1923
Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe	
540 545 550	
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG	1971
Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val	
555 560 565 570	
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC	2019
His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe	
575 580 585	
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAG GAC GCA CTG ACC	2067
Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr	
590 595 600	
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC	2115
Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly	
605 610 615	
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG	2163
Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met	
620 625 630	
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC	2211
Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn	
635 640 645 650	
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC	2259
Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly	
655 660 665	
ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC	2307
Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala	
670 675 680	
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG	2355
Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu	
685 690 695	
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG	2403
Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala	
700 705 710	
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC	2451
Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile	
715 720 725 730	
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG	2499
Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu	
735 740 745	
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG	2547
Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met	
750 755 760	

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CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG	2595
Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys	
765 770 775	
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG	2643
Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg	
780 785 790	
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT	2691
Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe	
795 800 805 810	
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC	2739
Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala	
815 820 825	
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT	2787
Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp	
830 835 840	
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG	2835
Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp	
845 850 855	
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT	2883
Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro	
860 865 870	
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC	2931
Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser	
875 880 885 890	
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC	2979
Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg	
895 900 905	
GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT	3027
Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile	
910 915 920	
GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC	3075
Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser	
925 930 935	
TGAGACTCCC CGCCCGCCCT CCTCTGCCCC CTCCCCCGCA GACAGACAGA CAGACGGACG	3135
GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG AGGAGCACCC	3195
CCAGCCTCCC CCAGGCTGCG CCGTCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC	3255
GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTTCT	3315
ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC AGATCCCTCG	3375
GTCAGCACCG TGGTGTGAGG CCCCCGAGG CGCCACCTG CCCAGTTAGC CCGGCCAAGG	3435
AACTGATGG GTCCTGCTGC TCGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG	3495
CCCACCCTGG GCCTCCCGTC CGTCCGCCCC CCCACCCCGC TGCCTGGCGG GCAGCCCCTG	3555
CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG	3615
GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG	3675
GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG	3735
CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTCGCC CCTCCTCGGG	3795

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CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCTC TTCTTGCGGC ACCGCCCACC 3855
 AAACACCCCG TCTGCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCACGGC 3915
 CGTCCCTGAC TTCCCAGCTG GCAGCGCCTC CCGCCGCTC GGGCCGCTC CTCCAGAATC 3975
 GAGAGGGCTG AGCCCCCTCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG GCCTCCCCGG 4035
 GGGTCCCCGG ACGCTGGCTC GGGACTGTCT TCAACCCTGC CCTGCACCTT GGGCACGGGA 4095
 GAGCGCCACC CGCCCGCCCC CGCCCTCGCT CCGGGTGCCT GACCGGCCCG CCACCTTGTA 4155
 CAGAACCCAGC ACTCCCAGGG CCGAGCGCG TGCCTTCCCC GTGCGCAGCC GCGCTCTGCC 4215
 CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCAACCCCC ACCTCCCGGT GTATGCAGTG 4275
 GTGATGCCTA AAGGAATGTC ACG 4298

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 938 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
 1 5 10 15
 Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
 20 25 30
 Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
 35 40 45
 Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
 50 55 60
 Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
 65 70 75 80
 Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
 85 90 95
 Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
 100 105 110
 Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
 115 120 125
 Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
 130 135 140
 Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
 145 150 155 160
 Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
 165 170 175
 Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu
 180 185 190

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Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu
 195 200 205
 Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser
 210 215 220
 Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met
 225 230 235 240
 GlyThr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser
 245 250 255
 Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile
 260 265 270
 Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val
 275 280 285
 Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro
 290 295 300
 Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu
 305 310 315 320
 Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly
 325 330 335
 Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser
 340 345 350
 Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn
 355 360 365
 Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly
 370 375 380
 Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile
 385 390 395 400
 Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser
 405 410 415
 Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys
 420 425 430
 Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg
 435 440 445
 His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile
 450 455 460
 Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala
 465 470 475 480
 Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys
 485 490 495
 Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met
 500 505 510
 Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu
 515 520 525
 Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys
 530 535 540

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Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser
 545 550 555 560
 Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met
 565 570 575
 Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn
 580 585 590
 Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp
 595 600 605
 Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro
 610 615 620
 Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala
 625 630 635 640
 Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val
 645 650 655
 Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu
 660 665 670
 Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser
 675 680 685
 Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg
 690 695 700
 His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala
 705 710 715 720
 Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu
 725 730 735
 Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu
 740 745 750
 Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp
 755 760 765
 Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe
 770 775 780
 Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser
 785 790 795 800
 Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val
 805 810 815
 Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe
 820 825 830
 Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met
 835 840 845
 Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp
 850 855 860
 Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe
 865 870 875 880
 Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser
 885 890 895

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Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln
 900 905 910

Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln
 915 920 925

Leu Gln Leu Cys Ser Arg His Arg Glu Ser
 930 935

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC	48
Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn	
1 5 10 15	
AAG CGC GGA CCC AAG	63
Lys Arg Gly Pro Lys	
20	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn	
1 5 10 15	
Lys Arg Gly Pro Lys	
20	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10038937.010402

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 189..3899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTAATAA GATTTGCCAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806
Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	
195 200 205	

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GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
			210					215					220			
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
		225					230					235				
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
	240					245					250					
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
255					260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275					280					285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
			290					295					300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
	320					325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
335					340					345					350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355					360					365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375					380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
	400					405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
415					420					425					430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435					440					445		
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
			450					455					460			
AAG	AAG	CTG	GCC	AGA	GTG	GTC	AAA	TTC	TCC	TAC	GAC	CTG	TAC	CTG	GTG	1622
Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	
		465					470					475				

ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG	1670
Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met	
480 485 490	
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC	1718
Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu	
495 500 505 510	
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT	1766
Thr Ile Asn Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe	
515 520 525	
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC	1814
Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val	
530 535 540	
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG	1862
Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met	
545 550 555	
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC	1910
Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe	
560 565 570	
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG	1958
Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys	
575 580 585 590	
AAG TCC GGG GGC CCA GCT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG	2006
Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu	
595 600 605	
TGG GCG CTG GTC TTC AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC	2054
Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly	
610 615 620	
ACC ACC AGC AAG ATC ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC	2102
Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Ala Val Ile	
625 630 635	
TTC CTC GCC AGA TAC ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG	2150
Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu	
640 645 650	
CAA TAC ATC GAC ACT GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG	2198
Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg	
655 660 665 670	
CCT CAA GAT CAG TAC CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC	2246
Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly	
675 680 685	
AGC ACG GAG CGG AAC ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC	2294
Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His	
690 695 700	
ATG GTC AAG TTC AAC CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC	2342
Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu	
705 710 715	
AAG ATG GGG AAG CTG GAT GCC TTC ATC TAT GAT GCT GCT GTC CTC AAC	2390
Lys Met Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Val Leu Asn	
720 725 730	
TAC ATG GCA GGC AAG GAC GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT	2438
Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser	
735 740 745 750	

GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC	2486
Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp	
755 760 765	
TCC CAC TGG AAG CGG GCC ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG	2534
Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly	
770 775 780	
GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC	2582
Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys	
785 790 795	
CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC	2630
Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn	
800 805 810	
ATG GCA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG	2678
Met Ala Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu	
815 820 825 830	
CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG	2726
Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser	
835 840 845	
GTG CCC AAC TCA TCC CAG CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC	2774
Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly	
850 855 860	
ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG	2822
Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg	
865 870 875	
CAG GCC AGC CCG GAC CTC ACG GCC AGC TCG GCC CAG GCC AGC GTG CTC	2870
Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu	
880 885 890	
AAG ATG CTG CAG GCA GCC CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC	2918
Lys Met Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser	
895 900 905 910	
AGC TCC CTG GAC CGC GCC ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC	2966
Ser Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly	
915 920 925	
CGC CGT GCG CCC CCA CCG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC	3014
Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro	
930 935 940	
AGC CCA TGC CTG CCC ACC CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG	3062
Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr	
945 950 955	
GGC TGG GGA CCG CCA GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT	3110
Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala	
960 965 970	
CCG CAG CCC CCG GGC CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC	3158
Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp	
975 980 985 990	
GTC TCC CGA GTG TCG CGC CGC CCA GCC TGG GAG GCG CCG TGG CCG GTG	3206
Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val	
995 1000 1005	
CGG ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG	3254
Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu	
1010 1015 1020	

204010 2658007

TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC 3302
 Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser
 1025 1030 1035

GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC 3350
 Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp
 1040 1045 1050

CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CCG CCG GAG GCC CTG CTG 3398
 Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu
 1055 1060 1065 1070

CAC GCG GCC TGG GCC CCG GGC TCG CGC CCG CGT CAC GCT TCC CTG CCC 3446
 His Ala Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro
 1075 1080 1085

AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG 3494
 Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly
 1090 1095 1100

TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGA CAC TCG GCC TGC AGG 3542
 Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg
 1105 1110 1115

CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC 3590
 Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala
 1120 1125 1130

TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG 3638
 Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln
 1135 1140 1145 1150

CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTT TGC TGG GGC GCT 3686
 His Val Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala
 1155 1160 1165

GTC TGT CCT CAC CTT CCA CCC TGT GCC AGC CAC GGC TCC TGG CTC TCC 3734
 Val Cys Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser
 1170 1175 1180

GGG GCC TGG GGC CCT CTG GGG CAC AGG GGC AGG ACT CTG GGG CTG GGC 3782
 Gly Ala Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly
 1185 1190 1195

ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGG GTA GCC 3830
 Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala
 1200 1205 1210

CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC 3878
 Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser
 1215 1220 1225 1230

AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA 3926
 Ser Leu Glu Ser Glu Val
 1235

GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG GCTTTTCTGG 3986

CTTCTACCAT GAAATCCTGG CCATGGGACC CCAGTGACAG ATGATGTCTT CCATGGTCAT 4046

CAGTGACCTC AGTAGCCTCA AATCATGGTG AGGGCTGGGC TTTTGCTGTC CTCTTCTCAC 4106

GCAGAGTTCT GCCAGGAGGG TGTGCTGTGG GGGTCAGACT CCTGAGGCTC TCCCTTCCCT 4166

GGGGCTAGCC AGTTACTGGT CATGCCTGCT GTGGGCATGG AGGCTGGAAC TTGTGGTTGA 4226

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GGCAGGGCCA TCCCGATCCT TGCTCTACCT GGCTAGAGTT TCTTCTCATC AGAGCACTGG 4286
 GACATTAAAC CCACCTTTTC CCAGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAG 4340

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
 1 5 10 15
 Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
 20 25 30
 Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
 35 40 45
 Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
 50 55 60
 Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
 65 70 75 80
 Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
 85 90 95
 Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
 100 105 110
 Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
 115 120 125
 Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
 130 135 140
 Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
 145 150 155 160
 Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
 165 170 175
 Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
 180 185 190
 Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
 195 200 205
 Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
 210 215 220
 Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
 225 230 235 240
 Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
 245 250 255
 Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
 260 265 270

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Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
 275 280 285
 Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
 290 295 300
 Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
 305 310 315 320
 Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
 325 330 335
 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
 340 345 350
 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu
 355 360 365
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr
 370 375 380
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser
 385 390 395 400
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val
 405 410 415
 Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro
 420 425 430
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro
 435 440 445
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys
 450 455 460
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn
 465 470 475 480
 Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly
 485 490 495
 Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile
 500 505 510
 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu
 515 520 525
 Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro
 530 535 540
 Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe
 545 550 555 560
 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr
 565 570 575
 Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser
 580 585 590
 Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala
 595 600 605
 Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr
 610 615 620

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Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu
 625 630 635 640
 Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr
 645 650 655
 Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln
 660 665 670
 Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr
 675 680 685
 Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val
 690 695 700
 Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met
 705 710 715 720
 Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met
 725 730 735
 Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys
 740 745 750
 Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His
 755 760 765
 Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly
 770 775 780
 Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn
 785 790 795 800
 Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala
 805 810 815
 Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val
 820 825 830
 Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro
 835 840 845
 Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr
 850 855 860
 Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala
 865 870 875 880
 Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Met
 885 890 895
 Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Ser Ser
 900 905 910
 Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg
 915 920 925
 Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro
 930 935 940
 Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp
 945 950 955 960
 Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln
 965 970 975

204070 7668E002

Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser
 980 985 990
 Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr
 995 1000 1005
 Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro
 1010 1015 1020
 Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg
 1025 1030 1035 1040
 Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro
 1045 1050 1055
 Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu His Ala
 1060 1065 1070
 Ala Trp Ala Arg Gly Ser Arg Pro Arg His Ala Ser Leu Pro Ser Ser
 1075 1080 1085
 Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr
 1090 1095 1100
 Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu
 1105 1110 1115 1120
 Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln
 1125 1130 1135
 Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val
 1140 1145 1150
 Cys Leu His Ala His Ala His Leu Pro Phe Cys Trp Gly Ala Val Cys
 1155 1160 1165
 Pro His Leu Pro Pro Cys Ala Ser His Gly Ser Trp Leu Ser Gly Ala
 1170 1175 1180
 Trp Gly Pro Leu Gly His Arg Gly Arg Thr Leu Gly Leu Gly Thr Gly
 1185 1190 1195 1200
 Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Arg Val Ala Arg Gly
 1205 1210 1215
 Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu
 1220 1225 1230
 Glu Ser Glu Val
 1235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..22

2040707.75588007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG
Ser Glu Ala Gln Pro Val Pro
1 5

24

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAAGGGGGT G

11

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4808 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: -

ATCATGGGAC CGGGTGAGCG CTGAGAATCG CGGCCGCAGC CATCAGCCCCT GGAGATGACC	60
AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT AGCCGCCCCC CGTGGGGGCG ATGCGGACAG CGCGGGACAG CCAGGGGAGC	180
GCGCTGGGGC CGCAGCATGC GGGAACCCG TAAACCCGGT GGCTGCTGAG GCGGCCGAGA	240
TGCTCGTGCG CGCAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGGACCGTC	300

204070-2668E007

AGTGGCGACT	ATG	GGC	AGA	GTG	GGC	TAT	TGG	ACC	CTG	CTG	GTG	CTG	CCG			349
	Met	Gly	Arg	Val	Gly	Tyr	Trp	Thr	Leu	Leu	Val	Leu	Pro			
	1				5					10						
GCC	CTT	CTG	GTC	TGG	CGC	GGT	CCG	GCG	CCG	AGC	GCG	GCG	GCG	GAG	AAG	397
Ala	Leu	Leu	Val	Trp	Arg	Gly	Pro	Ala	Pro	Ser	Ala	Ala	Ala	Glu	Lys	
	15					20					25					
GGT	CCC	CCC	GCG	CTA	AAT	ATT	GCG	GTG	ATG	CTG	GGT	CAC	AGC	CAC	GAC	445
Gly	Pro	Pro	Ala	Leu	Asn	Ile	Ala	Val	Met	Leu	Gly	His	Ser	His	Asp	
	30				35					40					45	
GTG	ACA	GAG	CGC	GAA	CTT	CGA	ACA	CTG	TGG	GGC	CCC	GAG	CAG	GCG	GCG	493
Val	Thr	Glu	Arg	Glu	Leu	Arg	Thr	Leu	Trp	Gly	Pro	Glu	Gln	Ala	Ala	
				50					55					60		
GGG	CTG	CCC	CTG	GAC	GTG	AAC	GTG	GTA	GCT	CTG	CTG	ATG	AAC	CGC	ACC	541
Gly	Leu	Pro	Leu	Asp	Val	Asn	Val	Val	Ala	Leu	Leu	Met	Asn	Arg	Thr	
			65					70					75			
GAC	CCC	AAG	AGC	CTC	ATC	ACG	CAC	GTG	TGC	GAC	CTC	ATG	TCC	GGG	GCA	589
Asp	Pro	Lys	Ser	Leu	Ile	Thr	His	Val	Cys	Asp	Leu	Met	Ser	Gly	Ala	
		80					85					90				
CGC	ATC	CAC	GGC	CTC	GTG	TTT	GGG	GAC	GAC	ACG	GAC	CAG	GAG	GCC	GTA	637
Arg	Ile	His	Gly	Leu	Val	Phe	Gly	Asp	Asp	Thr	Asp	Gln	Glu	Ala	Val	
	95					100					105					
GCC	CAG	ATG	CTG	GAT	TTT	ATC	TCC	TCC	CAC	ACC	TTC	GTC	CCC	ATC	TTG	685
Ala	Gln	Met	Leu	Asp	Phe	Ile	Ser	Ser	His	Thr	Phe	Val	Pro	Ile	Leu	
110					115					120					125	
GGC	ATT	CAT	GGG	GGC	GCA	TCT	ATG	ATC	ATG	GCT	GAC	AAG	GAT	CCG	ACG	733
Gly	Ile	His	Gly	Gly	Ala	Ser	Met	Ile	Met	Ala	Asp	Lys	Asp	Pro	Thr	
				130					135					140		
TCT	ACC	TTC	TTC	CAG	TTT	GGA	GCG	TCC	ATC	CAG	CAG	CAA	GCC	ACG	GTC	781
Ser	Thr	Phe	Phe	Gln	Phe	Gly	Ala	Ser	Ile	Gln	Gln	Gln	Ala	Thr	Val	
			145					150					155			
ATG	CTG	AAG	ATC	ATG	CAG	GAT	TAT	GAC	TGG	CAT	GTC	TTC	TCC	CTG	GTG	829
Met	Leu	Lys	Ile	Met	Gln	Asp	Tyr	Asp	Trp	His	Val	Phe	Ser	Leu	Val	
		160					165					170				
ACC	ACT	ATC	TTC	CCT	GGC	TAC	AGG	GAA	TTC	ATC	AGC	TTC	GTC	AAG	ACC	877
Thr	Thr	Ile	Phe	Pro	Gly	Tyr	Arg	Glu	Phe	Ile	Ser	Phe	Val	Lys	Thr	
	175					180					185					
ACA	GTG	GAC	AAC	AGC	TTT	GTG	GGC	TGG	GAC	ATG	CAG	AAT	GTG	ATC	ACA	925
Thr	Val	Asp	Asn	Ser	Phe	Val	Gly	Trp	Asp	Met	Gln	Asn	Val	Ile	Thr	
190					195					200					205	
CTG	GAC	ACT	TCC	TTT	GAG	GAT	GCA	AAG	ACA	CAA	GTC	CAG	CTG	AAG	AAG	973
Leu	Asp	Thr	Ser	Phe	Glu	Asp	Ala	Lys	Thr	Gln	Val	Gln	Leu	Lys	Lys	
				210					215					220		
ATC	CAC	TCT	TCT	GTC	ATC	TTG	CTC	TAC	TGT	TCC	AAA	GAC	GAG	GCT	GTT	1021
Ile	His	Ser	Ser	Val	Ile	Leu	Leu	Tyr	Cys	Ser	Lys	Asp	Glu	Ala	Val	
			225					230					235			
CTC	ATT	CTG	AGT	GAG	GCC	CGC	TCC	CTT	GGC	CTC	ACC	GGG	TAT	GAT	TTC	1069
Leu	Ile	Leu	Ser	Glu	Ala	Arg	Ser	Leu	Gly	Leu	Thr	Gly	Tyr	Asp	Phe	
		240					245					250				
TTC	TGG	ATT	GTC	CCC	AGC	TTG	GTC	TCT	GGG	AAC	ACG	GAG	CTC	ATC	CCA	1117
Phe	Trp	Ile	Val	Pro	Ser	Leu	Val	Ser	Gly	Asn	Thr	Glu	Leu	Ile	Pro	
	255					260					265					

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AAA Lys 270	GAG Glu	TTT Phe	CCA Pro	TCG Ser	GGG Gly 275	CTC Leu	ATT Ile	TCT Ser	GTC Val	TCC Ser 280	TAC Tyr	GAT Asp	GAC Asp	TGG Trp	GAC Asp 285	1165
TAC Tyr	AGC Ser	CTG Leu	GAG Glu	GCG Ala 290	AGA Arg	GTG Val	AGG Arg	GAC Asp	GGC Gly 295	ATT Ile	GGC Gly	ATC Ile	CTA Leu	ACC Thr 300	ACC Thr	1213
GCT Ala	GCA Ala	TCT Ser	TCT Ser 305	ATG Met	CTG Leu	GAG Glu	AAG Lys	TTC Phe 310	TCC Ser	TAC Tyr	ATC Ile	CCC Pro 315	GAG Glu 315	GCC Ala	AAG Lys	1261
GCC Ala	AGC Ser	TGC Cys 320	TAC Tyr	GGG Gly	CAG Gln	ATG Met	GAG Glu 325	AGG Arg	CCA Pro	GAG Glu	GTC Val 330	CCG Pro 330	ATG Met	CAC His	ACC Thr	1309
TTG Leu	CAC His 335	CCA Pro	TTT Phe	ATG Met	GTC Val 340	AAT Asn	GTT Val	ACA Thr	TGG Trp	GAT Asp	GGC Gly 345	AAA Lys	GAC Asp	TTA Leu	TCC Ser	1357
TTC Phe 350	ACT Thr	GAG Glu	GAA Glu	GGC Gly 355	TAC Tyr	CAG Gln	GTG Val	CAC His	CCC Pro 360	AGG Arg	CTG Leu	GTG Val	GTG Val	ATT Ile	GTG Val 365	1405
CTG Leu	AAC Asn	AAA Lys	GAC Asp 370	CGG Arg	GAA Glu	TGG Trp	GAA Glu	AAG Lys	GTG Val 375	GGC Gly	AAG Lys	TGG Trp	GAG Glu	AAC Asn 380	CAT His	1453
ACG Thr	CTG Leu	AGC Ser	CTG Leu 385	AGG Arg	CAC His	GCC Ala	GTG Val	TGG Trp 390	CCC Pro	AGG Arg	TAC Tyr	AAG Lys 395	TCC Ser 395	TTC Phe	TCC Ser	1501
GAC Asp	TGT Cys 400	GAG Glu	CCG Pro	GAT Asp	GAC Asp	AAC Asn	CAT His 405	CTC Leu	AGC Ser	ATC Ile	GTC Val 410	ACC Thr 410	CTG Leu	GAG Glu	GAG Glu	1549
GCC Ala	CCA Pro 415	TTC Phe	GTC Val	ATC Ile	GTG Val 420	GAA Glu	GAC Asp 420	ATA Ile	GAC Asp	CCC Pro 425	CTG Leu 425	ACC Thr	GAG Glu	ACG Thr	TGT Cys	1597
GTG Val 430	AGG Arg	AAC Asn	ACC Thr	GTG Val 435	CCA Pro	TGT Cys	CGG Arg	AAG Lys	TTC Phe 440	GTC Val 440	AAA Lys	ATC Ile	AAC Asn	AAT Asn	TCA Ser 445	1645
ACC Thr	AAT Asn	GAG Glu	GGG Gly 450	ATG Met	AAT Asn	GTG Val	AAG Lys	AAA Lys	TGC Cys 455	TGC Cys	AAG Lys	GGG Gly	TTC Phe	TGC Cys 460	ATT Ile	1693
GAT Asp	ATT Ile	CTG Leu	AAG Lys 465	AAG Lys	CTT Leu	TCC Ser	AGA Arg	ACT Thr 470	GTG Val	AAG Lys	TTT Phe	ACT Thr 475	TAC Tyr 475	GAC Asp	CTC Leu	1741
TAT Tyr	CTG Leu	GTG Val 480	ACC Thr	AAT Asn	GGG Gly	AAG Lys	CAT His 485	GGC Gly	AAG Lys	AAA Lys 490	GTT Val 490	AAC Asn	AAT Asn	GTG Val	TGG Trp	1789
AAT Asn	GGA Gly 495	ATG Met	ATC Ile	GGT Gly	GAA Glu 500	GTG Val 500	GTC Val	TAT Tyr	CAA Gln	CGG Arg 505	GCA Ala 505	GTC Val	ATG Met	GCA Ala	GTT Val	1837
GGC Gly 510	TCG Ser	CTC Leu	ACC Thr	ATC Ile 515	AAT Asn	GAG Glu 515	GAA Glu	CGT Arg	TCT Ser 520	GAA Glu 520	GTG Val 520	GTG Val	GAC Asp	TTC Phe	TCT Ser 525	1885
GTG Val	CCC Pro	TTT Phe	GTG Val 530	GAA Glu 530	ACG Thr	GGA Gly	ATC Ile	AGT Ser 535	GTC Val 535	ATG Met 535	GTT Val	TCA Ser	AGA Arg 540	AGT Ser 540	AAT Asn	1933

GGC	ACC	GTC	TCA	CCT	TCT	GCT	TTT	CTA	GAA	CCA	TTC	AGC	GCC	TCT	GTC	1981
Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Phe	Ser	Ala	Ser	Val	
		545						550					555			
TGG	GTG	ATG	ATG	TTT	GTG	ATG	CTG	CTC	ATT	GTT	TCT	GCC	ATA	GCT	GTT	2029
Trp	Val	Met	Met	Phe	Val	Met	Leu	Leu	Ile	Val	Ser	Ala	Ile	Ala	Val	
		560					565					570				
TGG	GTC	TTG	GAT	TAC	TCC	AGC	CCT	GTT	GGA	TAC	AAC	AGA	AAC	TTA	GCC	2077
Trp	Val	Leu	Asp	Tyr	Ser	Ser	Pro	Val	Gly	Tyr	Asn	Arg	Asn	Leu	Ala	
	575					580					585					
AAA	GGG	AAA	GCA	CCC	CAT	GGG	CCT	TCT	TTT	ACA	ATT	GGA	AAA	GCT	ATA	2125
Lys	Gly	Lys	Ala	Pro	His	Gly	Pro	Ser	Phe	Thr	Ile	Gly	Lys	Ala	Ile	
590					595				600						605	
TGG	CTT	CTT	TGG	GGC	CTG	GTG	TTC	AAT	AAC	TCC	GTG	CCT	GTC	CAG	AAT	2173
Trp	Leu	Leu	Trp	Gly	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Gln	Asn	
				610					615					620		
CCT	AAA	GGG	ACC	ACC	AGC	AAG	ATC	ATG	GTA	TCT	GTA	TGG	GCC	TTC	TTC	2221
Pro	Lys	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Ser	Val	Trp	Ala	Phe	Phe	
			625					630					635			
GCT	GTC	ATA	TTC	CTG	GCT	AGC	TAC	ACA	GCC	AAT	CTG	GCT	GCC	TTC	ATG	2269
Ala	Val	Ile	Phe	Leu	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	
		640					645					650				
ATC	CAA	GAG	GAA	TTT	GTG	GAC	CAA	GTG	ACC	GGC	CTC	AGT	GAC	AAA	AAG	2317
Ile	Gln	Glu	Glu	Phe	Val	Asp	Gln	Val	Thr	Gly	Leu	Ser	Asp	Lys	Lys	
	655					660					665					
TTT	CAG	AGA	CCT	CAT	GAC	TAT	TCC	CCA	CCT	TTT	CGA	TTT	GGG	ACA	GTG	2365
Phe	Gln	Arg	Pro	His	Asp	Tyr	Ser	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	
670					675					680					685	
CCT	AAT	GGA	AGC	ACG	GAG	AGA	AAC	ATT	CGG	AAT	AAC	TAT	CCC	TAC	ATG	2413
Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Asn	Asn	Tyr	Pro	Tyr	Met	
				690					695					700		
CAT	CAG	TAC	ATG	ACC	AAA	TTT	AAT	CAG	AAA	GGA	GTA	GAG	GAC	GCC	TTG	2461
His	Gln	Tyr	Met	Thr	Lys	Phe	Asn	Gln	Lys	Gly	Val	Glu	Asp	Ala	Leu	
			705					710					715			
GTC	AGC	CTG	AAA	ACG	GGG	AAG	CTG	GAC	GCT	TTC	ATC	TAC	GAT	GCC	GCA	2509
Val	Ser	Leu	Lys	Thr	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	
		720					725					730				
GTC	TTG	AAT	TAC	AAG	GCT	GGG	AGG	GAT	GAA	GGC	TGC	AAG	CTG	GTG	ACC	2557
Val	Leu	Asn	Tyr	Lys	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	
	735					740					745					
ATC	GGG	AGT	GGG	TAC	ATC	TTT	GCC	ACC	ACC	GGT	TAT	GGA	ATT	GCC	CTT	2605
Ile	Gly	Ser	Gly	Tyr	Ile	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	
750					755					760					765	
CAG	AAA	GGC	TCT	CCT	TGG	AAG	AGG	CAG	ATC	GAC	CTG	GCC	TTG	CTT	CAG	2653
Gln	Lys	Gly	Ser	Pro	Trp	Lys	Arg	Gln	Ile	Asp	Leu	Ala	Leu	Leu	Gln	
				770					775					780		
TTT	GTG	GGT	GAT	GGT	GAG	ATG	GAG	GAG	CTG	GAG	ACC	CTG	TGG	CTC	ACT	2701
Phe	Val	Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Thr	Leu	Trp	Leu	Thr	
			785					790					795			
GGG	ATC	TGC	CAC	AAC	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	CAG	CTG	GAC	2749
Gly	Ile	Cys	His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	
		800					805					810				

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ATT GAC AAC ATG GCG GGC GTA TTC TAC ATG CTG GCT GCC GCC ATG GCC Ile Asp Asn Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala 815 820 825	2797
CTT AGC CTC ATC ACC TTC ATC TGG GAG CAC CTC TTC TAC TGG AAG CTG Leu Ser Leu Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu 830 835 840 845	2845
CGC TTC TGT TTC ACC GGC GTG TGC TCC GAC CGG CCT GGG TTG CTC TTC Arg Phe Cys Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe 850 855 860	2893
TCC ATC AGC AGG GGC ATC TAC AGC TGC ATT CAT GGA GTG CAC ATT GAA Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu 865 870 875	2941
GAA AAG AAG AAG TCT CCA GAC TTC AAT CTG ACG GGA TCC CAG AGC AAC Glu Lys Lys Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn 880 885 890	2989
ATG TTA AAA CTC CTC CGG TCA GCC AAA AAC ATT TCC AGC ATG TCC AAC Met Leu Lys Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn 895 900 905	3037
ATG AAC TCC TCA AGA ATG GAC TCA CCC AAA AGA GCT GCT GAC TTC ATC Met Asn Ser Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile 910 915 920 925	3085
CAA AGA GGT TCC CTC ATC ATG GAC ATG GTT TCA GAT AAG GGG AAT TTG Gln Arg Gly Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu 930 935 940	3133
ATG TAC TCA GAC AAC AGG TCC TTT CAG GGG AAA GAG AGC ATT TTT GGA Met Tyr Ser Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly 945 950 955	3181
GAC AAC ATG AAC GAA CTC CAA ACA TTT GTG GCC AAC CGG CAG AAG GAT Asp Asn Met Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp 960 965 970	3229
AAC CTC AAT AAC TAT GTA TTC CAG GGA CAA CAT CCT CTT ACT CTC AAT Asn Leu Asn Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn 975 980 985	3277
GAG TCC AAC CCT AAC ACG GTG GAG GTG GCC GTG AGC ACA GAA TCC AAA Glu Ser Asn Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys 990 995 1000 1005	3325
GCG AAC TCT AGA CCC CGG CAG CTG TGG AAG AAA TCC GTG GAT TCC ATA Ala Asn Ser Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile 1010 1015 1020	3373
CGC CAG GAT TCA CTA TCC CAG AAT CCA GTC TCC CAG AGG GAT GAG GCA Arg Gln Asp Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala 1025 1030 1035	3421
ACA GCA GAG AAT AGG ACC CAC TCC CTA AAG AGC CCT AGG TAT CTT CCA Thr Ala Glu Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro 1040 1045 1050	3469
GAA GAG ATG GCC CAC TCT GAC ATT TCA GAA ACG TCA AAT CGG GCC ACG Glu Glu Met Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr 1055 1060 1065	3517
TGC CAC AGG GAA CCT GAC AAC AGT AAG AAC CAC AAA ACC AAG GAC AAC Cys His Arg Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn 1070 1075 1080 1085	3565

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TTT AAA AGG TCA GTG GCC TCC AAA TAC CCC AAG GAC TGT AGT GAG GTC	3613
Phe Lys Arg Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val	
1090 1095 1100	
GAG CGC ACC TAC CTG AAA ACC AAA TCA AGC TCC CCT AGA GAC AAG ATC	3661
Glu Arg Thr Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile	
1105 1110 1115	
TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC	3709
Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro	
1120 1125 1130	
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC	3757
Gln Phe Val Glu Asn Val Leu Pro Glu Asn Val Asp Phe Pro Asp	
1135 1140 1145	
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG	3805
Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu	
1150 1155 1160 1165	
CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC	3853
Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn	
1170 1175 1180	
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT	3901
Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly	
1185 1190 1195	
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC	3949
Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His	
1200 1205 1210	
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC	3997
Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr	
1215 1220 1225	
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC	4045
Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu	
1230 1235 1240 1245	
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC	4093
Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala	
1250 1255 1260	
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT	4141
Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu	
1265 1270 1275	
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT	4189
Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp	
1280 1285 1290	
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG	4237
Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg	
1295 1300 1305	
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC	4285
Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr	
1310 1315 1320 1325	
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC	4333
Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser	
1330 1335 1340	
TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC	4381
Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu	
1345 1350 1355	

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TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT 4429
 Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp
 1360 1365 1370
 GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC 4477
 Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His
 1375 1380 1385
 TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG 4525
 Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu
 1390 1395 1400 1405
 AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT 4573
 Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp
 1410 1415 1420
 GTG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT 4621
 Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn
 1425 1430 1435
 ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG 4669
 Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val
 1440 1445 1450
 TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT 4722
 Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val 146
 1455 1460
 TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC 4782
 AATAGTGCCC TGCTAAGAGG AAGGAG 4808

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu
 1 5 10 15
 Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro
 20 25 30
 Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu
 35 40 45
 Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro
 50 55 60
 Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys
 65 70 75 80
 Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His
 85 90 95
 Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met
 100 105 110
 Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His
 115 120 125

Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe
 130 135 140
 Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val Met Leu Lys
 145 150 155 160
 Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile
 165 170 175
 Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp
 180 185 190
 Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr
 195 200 205
 Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser
 210 215 220
 Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu
 225 230 235 240
 Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile
 245 250 255
 Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe
 260 265 270
 Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu
 275 280 285
 Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser
 290 295 300
 Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys
 305 310 315 320
 Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro
 325 330 335
 Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu
 340 345 350
 Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys
 355 360 365
 Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser
 370 375 380
 Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu
 385 390 395 400
 Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn
 420 425 430
 Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu
 435 440 445
 Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu
 450 455 460
 Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val
 465 470 475 480

10393 01040E
 201070 266807

Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp Asn Gly Met
 485 490 495
 Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu
 500 505 510
 Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe
 515 520 525
 Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val
 530 535 540
 Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met
 545 550 555 560
 Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu
 565 570 575
 Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys
 580 585 590
 Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu
 595 600 605
 Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly
 610 615 620
 Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile
 625 630 635 640
 Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu
 645 650 655
 Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg
 660 665 670
 Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly
 675 680 685
 Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr
 690 695 700
 Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu
 705 710 715 720
 Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn
 725 730 735
 Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser
 740 745 750
 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly
 755 760 765
 Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly
 770 775 780
 Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys
 785 790 795 800
 His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn
 805 810 815
 Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu
 820 825 830

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Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys
 835 840 845
 Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser
 850 855 860
 Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys
 865 870 875 880
 Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys
 885 890 895
 Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser
 900 905 910
 Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly
 915 920 925
 Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser
 930 935 940
 Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met
 945 950 955 960
 Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn
 965 970 975
 Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn
 980 985 990
 Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser
 995 1000 1005
 Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp
 1010 1015 1020
 Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu
 1025 1030 1035 1040
 Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met
 1045 1050 1055
 Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg
 1060 1065 1070
 Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg
 1075 1080 1085
 Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr
 1090 1095 1100
 Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile
 1105 1110 1115 1120
 Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val
 1125 1130 1135
 Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln
 1140 1145 1150
 Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn
 1155 1160 1165
 Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr
 1170 1175 1180

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Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His
 1185 1190 1195 1200
 Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser
 1205 1210 1215
 Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser
 1220 1225 1230
 Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile
 1235 1240 1245
 Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu
 1250 1255 1260
 Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln
 1265 1270 1275 1280
 Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val
 1285 1290 1295
 Asp Lys Pro Arg Glu⁻Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser
 1300 1305 1310
 Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu
 1315 1320 1325
 Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe
 1330 1335 1340
 Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp
 1345 1350 1355 1360
 His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg
 1365 1370 1375
 Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro
 1380 1385 1390
 Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr
 1395 1400 1405
 Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile
 1410 1415 1420
 Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser
 1425 1430 1435 1440
 Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu
 1445 1450 1455
 Met Pro Ser Ile Glu Ser Asp Val
 1460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCCGGCGCG GACTCTCTTC GCGGGCGCAG CGCCCCTTCC CCCTCGGACC 60
CTCCGGTGGA CATG 74

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 210..4664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGAATTTGC ATCTCTTCAA GACACAAGAT TAAACAAAA TTTACGCTAA ATTGGATTTT 60
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAAGAA 120
GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAATCTGT CCGTCTAGAG GTTTGGCTTC 180
TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT 233
Met Lys Pro Arg Ala Glu Cys Cys
1 5
TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC 281
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser
10 15 20
AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC 329
Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile
25 30 35 40
CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAA 377
Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys
45 50 55
GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC 425
Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala
60 65 70
ATG AAT GAG ACC GAC CCA AAG AGC ATC ATC ACC CGC ATC TGT GAT CTC 473
Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu
75 80 85
ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC 521
Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp
90 95 100
CAG GAA GCC ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC 569
Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu
105 110 115 120
ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT 617
Thr Pro Ile Leu Gly Ile His Gly Gly Ser Ser Met Ile Met Ala Asp
125 130 135

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AAG Lys	GAT Asp	GAA Glu	TCC Ser	TCC Ser	ATG Met	TTC Phe	TTC Phe	CAG Gln	TTT Phe	GGC Gly	CCA Pro	TCA Ser	ATT Ile	GAA Glu	CAG Gln	665
			140					145					150			
CAA Gln	GCT Ala	TCC Ser	GTA Val	ATG Met	CTC Leu	AAC Asn	ATC Ile	ATG Met	GAA Glu	GAA Glu	TAT Tyr	GAC Asp	TGG Trp	TAC Tyr	ATC Ile	713
			155				160					165				
TTT Phe	TCT Ser	ATC Ile	GTC Val	ACC Thr	ACC Thr	TAT Tyr	TTC Phe	CCT Pro	GGC Gly	TAC Tyr	CAG Gln	GAC Asp	TTT Phe	GTA Val	AAC Asn	761
		170				175					180					
AAG Lys	ATC Ile	CGC Arg	AGC Ser	ACC Thr	ATT Ile	GAG Glu	AAT Asn	AGC Ser	TTT Phe	GTG Val	GGC Gly	TGG Trp	GAG Glu	CTA Leu	GAG Glu	809
					190					195					200	
GAG Glu	GTC Val	CTC Leu	CTA Leu	CTG Leu	GAC Asp	ATG Met	TCC Ser	CTG Leu	GAC Asp	GAT Asp	GGA Gly	GAT Asp	TCT Ser	AAG Lys	ATC Ile	857
				205					210					215		
CAG Gln	AAT Asn	CAG Gln	CTC Leu	AAG Lys	AAA Lys	CTT Leu	CAA Gln	AGC Ser	CCC Pro	ATC Ile	ATT Ile	CTT Leu	CTT Leu	TAC Tyr	TGT Cys	905
			220				225						230			
ACC Thr	AAG Lys	GAA Glu	GAA Glu	GCC Ala	ACC Thr	TAC Tyr	ATC Ile	TTT Phe	GAA Glu	GTG Val	GCC Ala	AAC Asn	TCA Ser	GTA Val	GGG Gly	953
		235					240					245				
CTG Leu	ACT Thr	GGC Gly	TAT Tyr	GGC Gly	TAC Tyr	ACG Thr	TGG Trp	ATC Ile	GTG Val	CCC Pro	AGT Ser	CTG Leu	GTG Val	GCA Ala	GGG Gly	1001
		250				255					260					
GAT Asp	ACA Thr	GAC Asp	ACA Thr	GTG Val	CCT Pro	GCG Ala	GAG Glu	TTC Phe	CCC Pro	ACT Thr	GGG Gly	CTC Leu	ATC Ile	TCT Ser	GTA Val	1049
		265			270				275						280	
TCA Ser	TAT Tyr	GAT Asp	GAA Glu	TGG Trp	GAC Asp	TAT Tyr	GGC Gly	CTC Leu	CCC Pro	CCC Pro	AGA Arg	GTG Val	AGA Arg	GAT Asp	GGA Gly	1097
				285					290					295		
ATT Ile	GCC Ala	ATA Ile	ATC Ile	ACC Thr	ACT Thr	GCT Ala	GCT Ala	TCT Ser	GAC Asp	ATG Met	CTG Leu	TCT Ser	GAG Glu	CAC His	AGC Ser	1145
			300					305					310			
TTC Phe	ATC Ile	CCT Pro	GAG Glu	CCC Pro	AAA Lys	AGC Ser	AGT Ser	TGT Cys	TAC Tyr	AAC Asn	ACC Thr	CAC His	GAG Glu	AAG Lys	AGA Arg	1193
		315					320					325				
ATC Ile	TAC Tyr	CAG Gln	TCC Ser	AAT Asn	ATG Met	CTA Leu	AAT Asn	AGG Arg	TAT Tyr	CTG Leu	ATC Ile	AAT Asn	GTC Val	ACT Thr	TTT Phe	1241
		330				335					340					
GAG Glu	GGG Gly	AGG Arg	AAT Asn	TTG Leu	TCC Ser	TTC Phe	AGT Ser	GAA Glu	GAT Asp	GGC Gly	TAC Tyr	CAG Gln	ATG Met	CAC His	CCG Pro	1289
		345			350					355					360	
AAA Lys	CTG Leu	GTG Val	ATA Ile	ATT Ile	CTT Leu	CTG Leu	AAC Asn	AAG Lys	GAG Glu	AGG Arg	AAG Lys	TGG Trp	GAA Glu	AGG Arg	GTG Val	1337
				365					370				375			
GGG Gly	AAG Lys	TGG Trp	AAA Lys	GAC Asp	AAG Lys	TCC Ser	CTG Leu	CAG Gln	ATG Met	AAG Lys	TAC Tyr	TAT Tyr	GTG Val	TGG Trp	CCC Pro	1385
			380					385					390			
CGA Arg	ATG Met	TGT Cys	CCA Pro	GAG Glu	ACT Thr	GAA Glu	GAG Glu	CAG Gln	GAG Glu	GAT Asp	GAC Asp	CAT His	CTG Leu	AGC Ser	ATT Ile	1433
		395					400					405				

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GTG ACC CTG GAG GAG GCA CCA TTT GTC ATT GTG GAA AGT GTG GAC CCT	1481
Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Ser Val Asp Pro	
410 415 420	
CTG AGT GGA ACC TGC ATG AGG AAC ACA GTC CCC TGC CAA AAA CGC ATA	1529
Leu Ser Gly Thr Cys Met Arg Asn Thr Val Pro Cys Gln Lys Arg Ile	
425 430 435 440	
GTC ACT GAG AAT AAA ACA GAC GAG GAG CCG GGT TAC ATC AAA AAA TGC	1577
Val Thr Glu Asn Lys Thr Asp Glu Glu Pro Gly Tyr Ile Lys Lys Cys	
445 450 455	
TGC AAG GGG TTC TGT ATT GAC ATC CTT AAG AAA ATT TCT AAA TCT GTG	1625
Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Ile Ser Lys Ser Val	
460 465 470	
AAG TTC ACC TAT GAC CTT TAC CTG GTT ACC AAT GGC AAG CAT GGG AAG	1673
Lys Phe Thr Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys	
475 480 485	
AAA ATC AAT GGA ACC TGG AAT GGT ATG ATT GGA GAG GTG GTC ATG AAG	1721
Lys Ile Asn Gly Thr Trp Asn Gly Met Ile Gly Glu Val Val Met Lys	
490 495 500	
AGG GCC TAC ATG GCA GTG GGC TCA CTC ACC ATC AAT GAG GAA CGA TCG	1769
Arg Ala Tyr Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser	
505 510 515 520	
GAG GTG GTC GAC TTC TCT GTG CCC TTC ATA GAG ACA GGC ATC AGT GTC	1817
Glu Val Val Asp Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val	
525 530 535	
ATG GTG TCA CGC AGC AAT GGG ACT GTC TCA CCT TCT GCC TTC TTA GAG	1865
Met Val Ser Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu	
540 545 550	
CCA TTC AGC GCT GAC GTA TGG GTG ATG ATG TTT GTG ATG CTG CTC ATC	1913
Pro Phe Ser Ala Asp Val Trp Val Met Met Phe Val Met Leu Leu Ile	
555 560 565	
GTC TCA GCC GTG GCT GTC TTT GTC TTT GAG TAC TTC AGC CCT GTG GGT	1961
Val Ser Ala Val Ala Val Phe Val Phe Glu Tyr Phe Ser Pro Val Gly	
570 575 580	
TAT AAC AGG TGC CTC GCT GAT GGC AGA GAG CCT GGT GGA CCC TCT TTC	2009
Tyr Asn Arg Cys Leu Ala Asp Gly Arg Glu Pro Gly Gly Pro Ser Phe	
585 590 595 600	
ACC ATC GGC AAA GCT ATT TGG TTG CTC TGG GGT CTG GTG TTT AAC AAC	2057
Thr Ile Gly Lys Ala Ile Trp Leu Leu Trp Gly Leu Val Phe Asn Asn	
605 610 615	
TCC GTA CCT GTG CAG AAC CCA AAG GGG ACC ACC TCC AAG ATC ATG GTG	2105
Ser Val Pro Val Gln Asn Pro Lys Gly Thr Thr Ser Lys Ile Met Val	
620 625 630	
TCA GTG TGG GCC TTC TTT GCT GTC ATC TTC CTG GCC AGC TAC ACT GCC	2153
Ser Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala	
635 640 645	
AAC TTA GCT GCC TTC ATG ATC CAA GAG GAA TAT GTG GAC CAG GTT TCT	2201
Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Gln Val Ser	
650 655 660	
GGC CTG AGC GAC AAA AAG TTC CAG AGA CCT AAT GAC TTC TCA CCC CCT	2249
Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Asn Asp Phe Ser Pro Pro	
665 670 675 680	

TTC CGC TTT GGG ACC GTG CCC AAC GGC AGC ACA GAG AGA AAT ATT CGC	2297
Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg	
685 690 695	
AAT AAC TAT GCA GAA ATG CAT GCC TAC ATG GGA AAG TTC AAC CAG AGG	2345
Asn Asn Tyr Ala Glu Met His Ala Tyr Met Gly Lys Phe Asn Gln Arg	
700 705 710	
GGT GTA GAT GAT GCA TTG CTC TCC CTG AAA ACA GGG AAA CTG GAT GCC	2393
Gly Val Asp Asp Ala Leu Leu Ser Leu Lys Thr Gly Lys Leu Asp Ala	
715 720 725	
TTC ATC TAT GAT GCA GCA GTG CTG AAC TAT ATG GCA GGC AGA GAT GAA	2441
Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Arg Asp Glu	
730 735 740	
GGC TGC AAG CTG GTG ACC ATT GGC AGT GGG AAG GTC TTT GCT TCC ACT	2489
Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Ser Thr	
745 750 755 760	
GGC TAT GGC ATT GCC ATC CAA AAA GAT TCT GGG TGG AAG CGC CAG GTG	2537
Gly Tyr Gly Ile Ala Ile Gln Lys Asp Ser Gly Trp Lys Arg Gln Val	
765 770 775	
GAC CTT GCT ATC CTG CAG CTC TTT GGA GAT GGG GAG ATG GAA GAA CTG	2585
Asp Leu Ala Ile Leu Gln Leu Phe Gly Asp Gly Glu Met Glu Glu Leu	
780 785 790	
GAA GCT CTC TGG CTC ACT GGC ATT TGT CAC AAT GAG AAG AAT GAG GTC	2633
Glu Ala Leu Trp Leu Thr Gly Ile Cys His Asn Glu Lys Asn Glu Val	
795 800 805	
ATG AGC AGC CAG CTG GAC ATT GAC AAC ATG GCA GGG GTC TTC TAC ATG	2681
Met Ser Ser Gln Leu Asp Ile Asp Asn Met Ala Gly Val Phe Tyr Met	
810 815 820	
TTG GGG GCG GCC ATG GCT CTC AGC CTC ATC ACC TTC ATC TGC GAA CAC	2729
Leu Gly Ala Ala Met Ala Leu Ser Leu Ile Thr Phe Ile Cys Glu His	
825 830 835 840	
CTT TTC TAT TGG CAG TTC CGA CAT TGC TTT ATG GGT GTC TGT TCT GGC	2777
Leu Phe Tyr Trp Gln Phe Arg His Cys Phe Met Gly Val Cys Ser Gly	
845 850 855	
AAG CCT GGC ATG GTC TTC TCC ATC AGC AGA GGT ATC TAC AGC TGC ATC	2825
Lys Pro Gly Met Val Phe Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile	
860 865 870	
CAT GGG GTG GCG ATC GAG GAG CGC CAG TCT GTA ATG AAC TCC CCC ACC	2873
His Gly Val Ala Ile Glu Glu Arg Gln Ser Val Met Asn Ser Pro Thr	
875 880 885	
GCA ACC ATG AAC AAC ACA CAC TCC AAC ATC CTG CGC CTG CTG CGC ACG	2921
Ala Thr Met Asn Asn Thr His Ser Asn Ile Leu Arg Leu Leu Arg Thr	
890 895 900	
GCC AAG AAC ATG GCT AAC CTG TCT GGT GTG AAT GGC TCA CCG CAG AGC	2969
Ala Lys Asn Met Ala Asn Leu Ser Gly Val Asn Gly Ser Pro Gln Ser	
905 910 915 920	
GCC CTG GAC TTC ATC CGA CGG GAG TCA TCC GTC TAT GAC ATC TCA GAG	3017
Ala Leu Asp Phe Ile Arg Arg Glu Ser Ser Val Tyr Asp Ile Ser Glu	
925 930 935	
CAC CGC CGC AGC TTC ACG CAT TCT GAC TGC AAA TCC TAC AAC AAC CCG	3065
His Arg Arg Ser Phe Thr His Ser Asp Cys Lys Ser Tyr Asn Asn Pro	
940 945 950	

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CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA	3113
Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg	
955 960 965	
ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC	3161
Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His	
970 975 980	
TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC	3209
Tyr His His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile	
985 990 995 1000	
GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG	3257
Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg	
1005 1010 1015	
TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC	3305
Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His	
1020 1025 1030	
AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC	3353
Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg	
1035 1040 1045	
TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA	3401
Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser	
1050 1055 1060	
ACC CAC ACC GTC ACC TAT GGG AAC ATC GAG GGC AAT GCC GCC AAG AGG	3449
Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg	
1065 1070 1075 1080	
CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC	3497
Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala	
1085 1090 1095	
AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA	3545
Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg	
1100 1105 1110	
CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG	3593
Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly	
1115 1120 1125	
CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC	3641
Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro	
1130 1135 1140	
CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT	3689
His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp	
1145 1150 1155 1160	
GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG	3737
Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Gly Pro Cys Thr Asn Arg	
1165 1170 1175	
TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG	3785
Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly	
1180 1185 1190	
GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC	3833
Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp	
1195 1200 1205	
CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC	3881
Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn	
1210 1215 1220	

204070 2E68E001

TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC 3929
 Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile
 1225 1230 1235 1240
 CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC AGT GAG 3977
 Arg Cys Glu Ala Cys Lys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu
 1245 1250 1255
 GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG 4025
 Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val
 1260 1265 1270
 ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC 4073
 Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser
 1275 1280 1285
 AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC 4121
 Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Gln His Ser Tyr
 1290 1295 1300
 GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC 4169
 Asp Thr Phe Val Asp Leu Gln Lys Glu Glu Ala Ala Leu Ala Pro Arg
 1305 1310 1315 1320
 AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC 4217
 Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr
 1325 1330 1335
 GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC 4265
 Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn
 1340 1345 1350
 AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC CAC AAC AAC CCC GGC 4313
 Lys Ser Ser Val Pro Thr Ala Gly His His His His Asn Asn Pro Gly
 1355 1360 1365
 GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA 4361
 Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln
 1370 1375 1380
 AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC 4409
 Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly
 1385 1390 1395 1400
 AGC AAA TCC TAC TTC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA 4457
 Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys
 1405 1410 1415
 GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG 4505
 Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser
 1420 1425 1430
 GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA 4553
 Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile
 1435 1440 1445
 GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT 4601
 Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala
 1450 1455 1460
 TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT 4649
 Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile
 1465 1470 1475 1480
 GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG 4701
 Glu Ser Asp Val

TAAGGCTGTG GGTGCGGTGA TGCGCATGTC ACGGAGGGTG ACGGGGGTGA ACTTGGTTCC 4761
 CATTGTCTCC TTTCTTGTTT TAATTTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG 4821
 GGGCAACCCT GGTGACCAGC ACCATCTCTC CTCCTTTTCA CAGTTCTCTC CTTCTTCCCC 4881
 CCGCTGTCAG CCATTCCTGT TCCCATGAGA TGATGCCATG GGCCCTCTCA GCAGGGGAGG 4941
 GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCCTCC TGGTGTGGAA GAGCTCCTTG 5001
 ATATCCTCTT TGAGTGAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC 5061
 TTTTCCCAA CTGATCTTTT CATTAGGTG AGGAAGCAAA AGCATCTATG TGAGACCATT 5121
 TAGCACACTG CTTGTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT 5181
 CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTTA TATATAAGCC 5241
 CAAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC 5301
 ATTGGTGGCA GAGTGGATTC TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG 5361
 TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTTCATGCA CACTTGCACC 5421
 CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT 5481
 CTTCAAGACA CAAGATTAAA ACAAATTTA CGCTAAATTG GATTTTAAAT TATCTTC 5538

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Lys Pro Arg Ala Glu Cys Cys Ser Pro Lys Phe Trp Leu Val Leu
 1 5 10 15
 Ala Val Leu Ala Val Ser Gly Ser Arg Ala Arg Ser Gln Lys Ser Pro
 20 25 30
 Pro Ser Ile Gly Ile Ala Val Ile Leu Val Gly Thr Ser Asp Glu Val
 35 40 45
 Ala Ile Lys Asp Ala His Glu Lys Asp Asp Phe His His Leu Ser Val
 50 55 60
 Val Pro Arg Val Glu Leu Val Ala Met Asn Glu Thr Asp Pro Lys Ser
 65 70 75 80
 Ile Ile Thr Arg Ile Cys Asp Leu Met Ser Asp Arg Lys Ile Gln Gly
 85 90 95
 Val Val Phe Ala Asp Asp Thr Asp Gln Glu Ala Ile Ala Gln Ile Leu
 100 105 110
 Asp Phe Ile Ser Ala Gln Thr Leu Thr Pro Ile Leu Gly Ile His Gly
 115 120 125
 Gly Ser Ser Met Ile Met Ala Asp Lys Asp Glu Ser Ser Met Phe Phe
 130 135 140

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Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile
 145 150 155 160
 Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe
 165 170 175
 Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn
 180 185 190
 Ser Phe Val Gly Trp Glu Leu Glu Glu Val Leu Leu Leu Asp Met Ser
 195 200 205
 Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln
 210 215 220
 Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile
 225 230 235 240
 Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp
 245 250 255
 Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu
 260 265 270
 Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly
 275 280 285
 Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Thr Thr Ala Ala
 290 295 300
 Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser
 305 310 315 320
 Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn
 325 330 335
 Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser
 340 345 350
 Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn
 355 360 365
 Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu
 370 375 380
 Gln Met Lys Tyr Tyr Val Trp Pro Arg Met Cys Pro Glu Thr Glu Glu
 385 390 395 400
 Gln Glu Asp Asp His Leu Ser Ile Val Thr Leu Glu Glu Ala Pro Phe
 405 410 415
 Val Ile Val Glu Ser Val Asp Pro Leu Ser Gly Thr Cys Met Arg Asn
 420 425 430
 Thr Val Pro Cys Gln Lys Arg Ile Val Thr Glu Asn Lys Thr Asp Glu
 435 440 445
 Glu Pro Gly Tyr Ile Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile
 450 455 460
 Leu Lys Lys Ile Ser Lys Ser Val Lys Phe Thr Tyr Asp Leu Tyr Leu
 465 470 475 480
 Val Thr Asn Gly Lys His Gly Lys Lys Ile Asn Gly Thr Trp Asn Gly
 485 490 495

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Met Ile Gly Glu Val Val Met Lys Arg Ala Tyr Met Ala Val Gly Ser
 500 505 510
 Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro
 515 520 525
 Phe Ile Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr
 530 535 540
 Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Asp Val Trp Val
 545 550 555 560
 Met Met Phe Val Met Leu Leu Ile Val Ser Ala Val Ala Val Phe Val
 565 570 575
 Phe Glu Tyr Phe Ser Pro Val Gly Tyr Asn Arg Cys Leu Ala Asp Gly
 580 585 590
 Arg Glu Pro Gly Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu
 595 600 605
 Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys
 610 615 620
 Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val
 625 630 635 640
 Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln
 645 650 655
 Glu Glu Tyr Val Asp Gln Val Ser Gly Leu Ser Asp Lys Lys Phe Gln
 660 665 670
 Arg Pro Asn Asp Phe Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn
 675 680 685
 Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Ala Glu Met His Ala
 690 695 700
 Tyr Met Gly Lys Phe Asn Gln Arg Gly Val Asp Asp Ala Leu Leu Ser
 705 710 715 720
 Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu
 725 730 735
 Asn Tyr Met Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly
 740 745 750
 Ser Gly Lys Val Phe Ala Ser Thr Gly Tyr Gly Ile Ala Ile Gln Lys
 755 760 765
 Asp Ser Gly Trp Lys Arg Gln Val Asp Leu Ala Ile Leu Gln Leu Phe
 770 775 780
 Gly Asp Gly Glu Met Glu Glu Leu Glu Ala Leu Trp Leu Thr Gly Ile
 785 790 795 800
 Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp
 805 810 815
 Asn Met Ala Gly Val Phe Tyr Met Leu Gly Ala Ala Met Ala Leu Ser
 820 825 830
 Leu Ile Thr Phe Ile Cys Glu His Leu Phe Tyr Trp Gln Phe Arg His
 835 840 845

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Cys Phe Met Gly Val Cys Ser Gly Lys Pro Gly Met Val Phe Ser Ile
 850 855 860
 Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val Ala Ile Glu Glu Arg
 865 870 875 880
 Gln Ser Val Met Asn Ser Pro Thr Ala Thr Met Asn Asn Thr His Ser
 885 890 895
 Asn Ile Leu Arg Leu Leu Arg Thr Ala Lys Asn Met Ala Asn Leu Ser
 900 905 910
 Gly Val Asn Gly Ser Pro Gln Ser Ala Leu Asp Phe Ile Arg Arg Glu
 915 920 925
 Ser Ser Val Tyr Asp Ile Ser Glu His Arg Arg Ser Phe Thr His Ser
 930 935 940
 Asp Cys Lys Ser Tyr Asn Asn Pro Pro Cys Glu Glu Asn Leu Phe Ser
 945 950 955 960
 Asp Tyr Ile Ser Glu Val Glu Arg Thr Phe Gly Asn Leu Gln Leu Lys
 965 970 975
 Asp Ser Asn Val Tyr Gln Asp His Tyr His His His His Arg Pro His
 980 985 990
 Ser Ile Gly Ser Ala Ser Ser Ile Asp Gly Leu Tyr Asp Cys Asp Asn
 995 1000 1005
 Pro Pro Phe Thr Thr Gln Ser Arg Ser Ile Ser Lys Lys Pro Leu Asp
 1010 1015 1020
 Ile Gly Leu Pro Ser Ser Lys His Ser Gln Leu Ser Asp Leu Tyr Gly
 1025 1030 1035 1040
 Lys Phe Ser Phe Lys Ser Asp Arg Tyr Ser Gly His Asp Asp Leu Ile
 1045 1050 1055
 Arg Ser Asp Val Ser Asp Ile Ser Thr His Thr Val Thr Tyr Gly Asn
 1060 1065 1070
 Ile Glu Gly Asn Ala Ala Lys Arg Arg Lys Gln Gln Tyr Lys Asp Ser
 1075 1080 1085
 Leu Lys Lys Arg Pro Ala Ser Ala Lys Ser Arg Arg Glu Phe Asp Glu
 1090 1095 1100
 Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys
 1105 1110 1115 1120
 Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln
 1125 1130 1135
 Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr
 1140 1145 1150
 Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser
 1155 1160 1165
 Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly
 1170 1175 1180
 Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn
 1185 1190 1195 1200

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Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg
 1205 1210 1215
 Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln
 1220 1225 1230
 Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala
 1235 1240 1245
 Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp
 1250 1255 1260
 Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys
 1265 1270 1275 1280
 Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn
 1285 1290 1295
 Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys
 1300 1305 1310
 Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly
 1315 1320 1325
 Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala
 1330 1335 1340
 Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly
 1345 1350 1355 1360
 His His His His Asn Asn Pro Gly Gly Gly Tyr Met Leu Ser Lys Ser
 1365 1370 1375
 Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly
 1380 1385 1390
 Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln
 1395 1400 1405
 Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu
 1410 1415 1420
 Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala
 1425 1430 1435 1440
 Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val
 1445 1450 1455
 Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His
 1460 1465 1470
 Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val
 1475 1480

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

204070 266800

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 485..4495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
CCGCCACCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCCA	180
GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCGGCTTG CCGTTGTGCG CACCACCACT GCCGCCGCC CGGGGCCTGC CCCCACATC	360
GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTCC GGTCTTGGCC	420
CCCCGCCAT CCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCCGCA	480
GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG	529
Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	
1 5 10 15	
ATG CTG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG	577
Met Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu	
20 25 30	
GCG CCG GGG CCG GGC GGG GCC GGT GGG CCC GGC GGC GGC CTC GGC GGC	625
Ala Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly	
35 40 45	
GCG CCG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG	673
Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	
50 55 60	
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC	721
Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser	
65 70 75	
CCG GGC CTA GAC GTG CCG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC	769
Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	
80 85 90 95	
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC	817
Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg	
100 105 110	
GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCG CCC GCC GTC GCG	865
Val His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala	
115 120 125	
CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC	913
Pro Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser	
130 135 140	
GAG CAC GGC GGC GCC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC	961
Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser	
145 150 155	
ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC	1009
Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile	
160 165 170 175	

204010 2653007

TTT	GAG	GTG	CTG	GAG	GAG	TAT	GAC	TGG	ACG	TCC	TTT	GTA	GCC	GTG	ACC	1057
Phe	Glu	Val	Leu	Glu	Glu	Tyr	Asp	Trp	Thr	Ser	Phe	Val	Ala	Val	Thr	
			180						185					190		
ACT	CGT	GCC	CCT	GGC	CAC	CGG	GCC	TTC	CTG	TCC	TAC	ATT	GAG	GTG	CTG	1105
Thr	Arg	Ala	Pro	Gly	His	Arg	Ala	Phe	Leu	Ser	Tyr	Ile	Glu	Val	Leu	
			195					200					205			
ACT	GAC	GGC	AGT	CTG	GTG	GGC	TGG	GAG	CAC	CGC	GGA	GCG	CTG	ACG	CTG	1153
Thr	Asp	Gly	Ser	Leu	Val	Gly	Trp	Glu	His	Arg	Gly	Ala	Leu	Thr	Leu	
		210					215					220				
GAC	CCT	GGG	GCG	GGC	GAG	GCC	GTG	CTC	AGT	GCC	CAG	CTC	GCG	AGT	GTC	1201
Asp	Pro	Gly	Ala	Gly	Glu	Ala	Val	Leu	Ser	Ala	Gln	Leu	Arg	Ser	Val	
	225					230					235					
AGC	GCG	CAG	ATC	CGC	CTG	CTC	TTC	TGC	GCC	CGA	GAG	GAG	GCC	GAG	CCC	1249
Ser	Ala	Gln	Ile	Arg	Leu	Leu	Phe	Cys	Ala	Arg	Glu	Glu	Ala	Glu	Pro	
	240				245				250						255	
GTG	TTC	CGC	GCA	GCT	GAG	GAG	GCT	GGC	CTC	ACT	GGA	TCT	GGC	TAC	GTC	1297
Val	Phe	Arg	Ala	Ala	Glu	Glu	Ala	Gly	Leu	Thr	Gly	Ser	Gly	Tyr	Val	
				260					265					270		
TGG	TTC	ATG	GTG	GGG	CCC	CAG	CTG	GCT	GGA	GGC	GGG	GGC	TCT	GGG	GCC	1345
Trp	Phe	Met	Val	Gly	Pro	Gln	Leu	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Ala	
			275					280					285			
CCT	GGT	GAG	CCC	CCT	CTT	CTG	CCA	GGA	GGC	GCC	CCC	CTG	CCT	GCC	GGG	1393
Pro	Gly	Glu	Pro	Pro	Leu	Leu	Pro	Gly	Gly	Ala	Pro	Leu	Pro	Ala	Gly	
		290					295					300				
CTG	TTT	GCA	GTG	CGC	TCG	GCT	GGC	TGG	CGG	GAT	GAC	CTG	GCT	CGG	CGA	1441
Leu	Phe	Ala	Val	Arg	Ser	Ala	Gly	Trp	Arg	Asp	Asp	Leu	Ala	Arg	Arg	
	305					310					315					
GTG	GCA	GCT	GGC	GTG	GCC	GTA	GTG	GCC	AGA	GGT	GCC	CAG	GCC	CTG	CTG	1489
Val	Ala	Ala	Gly	Val	Ala	Val	Val	Ala	Arg	Gly	Ala	Gln	Ala	Leu	Leu	
	320				325				330					335		
CGT	GAT	TAT	GGT	TTC	CTT	CCT	GAG	CTC	GGC	CAC	GAC	TGT	CGC	GCC	CAG	1537
Arg	Asp	Tyr	Gly	Phe	Leu	Pro	Glu	Leu	Gly	His	Asp	Cys	Arg	Ala	Gln	
				340					345					350		
AAC	CGC	ACC	CAC	CGC	GGG	GAG	AGT	CTG	CAT	AGG	TAC	TTC	ATG	AAC	ATC	1585
Asn	Arg	Thr	His	Arg	Gly	Glu	Ser	Leu	His	Arg	Tyr	Phe	Met	Asn	Ile	
			355					360					365			
ACG	TGG	GAT	AAC	CGG	GAT	TAC	TCC	TTC	AAT	GAG	GAC	GGC	TTC	CTA	GTG	1633
Thr	Trp	Asp	Asn	Arg	Asp	Tyr	Ser	Phe	Asn	Glu	Asp	Gly	Phe	Leu	Val	
		370				375						380				
AAC	CCC	TCC	CTG	GTG	GTC	ATC	TCC	CTC	ACC	AGA	GAC	AGG	ACG	TGG	GAG	1681
Asn	Pro	Ser	Leu	Val	Val	Ile	Ser	Leu	Thr	Arg	Asp	Arg	Thr	Trp	Glu	
	385					390					395					
GTG	GTG	GGC	AGC	TGG	GAG	CAG	CAG	ACG	CTC	CGC	CTC	AAG	TAC	CCG	CTG	1729
Val	Val	Gly	Ser	Trp	Glu	Gln	Gln	Thr	Leu	Arg	Leu	Lys	Tyr	Pro	Leu	
	400				405				410					415		
TGG	TCC	CGC	TAT	GGT	CGC	TTC	CTG	CAG	CCA	GTG	GAC	GAC	ACG	CAG	CAC	1777
Trp	Ser	Arg	Tyr	Gly	Arg	Phe	Leu	Gln	Pro	Val	Asp	Asp	Thr	Gln	His	
				420					425					430		
CTC	GCG	GTG	GCC	ACG	CTG	GAG	GAA	AGG	CCG	TTT	GTC	ATC	GTG	GAG	CCT	1825
Leu	Ala	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	Glu	Pro	
			435					440					445			

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GCA	GAC	CCT	ATC	AGC	GGC	ACC	TGC	ATC	CGA	GAC	TCC	GTC	CCC	TGC	CGG	1873
Ala	Asp	Pro	Ile	Ser	Gly	Thr	Cys	Ile	Arg	Asp	Ser	Val	Pro	Cys	Arg	
		450					455					460				
AGC	CAG	CTC	AAC	CGA	ACC	CAC	AGC	CCT	CCA	CCG	GAT	GCC	CCC	CGC	CCG	1921
Ser	Gln	Leu	Asn	Arg	Thr	His	Ser	Pro	Pro	Pro	Asp	Ala	Pro	Arg	Pro	
	465					470					475					
GAA	AAG	CGC	TGC	TGC	AAG	GGT	TTC	TGC	ATC	GAC	ATT	CTG	AAG	CGG	CTG	1969
Glu	Lys	Arg	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Arg	Leu	
	480				485					490					495	
GCG	CAT	ACC	ATC	GGC	TTC	AGC	TAC	GAC	CTC	TAC	CTG	GTC	ACC	AAT	GGC	2017
Ala	His	Thr	Ile	Gly	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	
				500					505					510		
AAG	CAC	GGA	AAG	AAG	ATC	GAT	GGC	GTC	TGG	AAC	GGC	ATG	ATC	GGG	GAG	2065
Lys	His	Gly	Lys	Lys	Ile	Asp	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	Glu	
			515					520					525			
GTG	TTC	TAC	CAG	CGC	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	ACC	ATC	AAC	2113
Val	Phe	Tyr	Gln	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	Asn	
		530					535					540				
GAG	GAG	CGC	TCC	GAG	ATC	GTG	GAC	TTC	TCC	GTC	CCC	TTC	GTG	GAG	ACC	2161
Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	Thr	
	545					550					555					
GGC	ATC	AGC	GTC	ATG	GTG	GCG	CGC	AGC	AAT	GGC	ACG	GTG	TCC	CCC	TCG	2209
Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	
	560				565					570					575	
GCC	TTC	CTC	GAG	CCC	TAC	AGC	CCC	GCC	GTG	TGG	GTG	ATG	ATG	TTC	GTC	2257
Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe	Val	
				580					585					590		
ATG	TGC	CTC	ACT	GTG	GTC	GCC	GTC	ACT	GTT	TTC	ATC	TTC	GAG	TAC	CTC	2305
Met	Cys	Leu	Thr	Val	Val	Ala	Val	Thr	Val	Phe	Ile	Phe	Glu	Tyr	Leu	
			595					600					605			
AGT	CCT	GTT	GGT	TAC	AAC	CGC	AGC	CTG	GCC	ACG	GGC	AAG	CGC	CCT	GGC	2353
Ser	Pro	Val	Gly	Tyr	Asn	Arg	Ser	Leu	Ala	Thr	Gly	Lys	Arg	Pro	Gly	
		610					615					620				
GGT	TCA	ACC	TTC	ACC	ATT	GGG	AAA	TCC	ATC	TGG	CTG	CTC	TGG	GCC	CTG	2401
Gly	Ser	Thr	Phe	Thr	Ile	Gly	Lys	Ser	Ile	Trp	Leu	Leu	Trp	Ala	Leu	
		625				630					635					
GTG	TTC	AAT	AAT	TCG	GTG	CCC	GTG	GAG	AAC	CCC	CGG	GGA	ACC	ACC	AGC	2449
Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	
					645					650					655	
AAA	ATC	ATG	GTG	CTG	GTG	TGG	GCC	TTC	TTC	GCC	GTC	ATC	TTC	CTC	GCC	2497
Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	
				660					665					670		
AGC	TAC	ACA	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAG	GAG	GAG	TAC	GTG	2545
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Glu	Tyr	Val	
				675				680						685		
GAT	ACT	GTG	TCT	GGG	CTC	AGT	GAC	CGC	AAG	TTC	CAG	AGG	CCC	CAG	GAG	2593
Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Arg	Lys	Phe	Gln	Arg	Pro	Gln	Glu	
		690					695					700				
CAG	TAC	CCG	CCC	CTG	AAG	TTT	GGG	ACC	GTG	CCC	AAC	GGC	TCC	ACG	GAG	2641
Gln	Tyr	Pro	Pro	Leu	Lys	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	
		705				710					715					

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AAG AAC ATC CGC AGC AAC TAT CCC GAC ATG CAC AGC TAC ATG GTG CGC Lys Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg 720 725 730 735	2689
TAC AAC CAG CCC CGC GTA GAG GAA GCG CTC ACT CAG CTC AAG GCA GGG Tyr Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly 740 745 750	2737
AAG CTG GAC GCC TTC ATC TAC GAT GCT GCA GTG CTC AAT TAC ATG GCC Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala 755 760 765	2785
CGC AAG GAC GAG GGC TGC AAG CTT GTC ACC ATC GGC TCC GGC AAG GTC Arg Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val 770 775 780	2833
TTC GCC ACG ACA GGC TAT GGC ATC GCC CTG CAC AAG GGC TCC CGC TGG Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp 785 790 795	2881
AAG CGG CCC ATC GAG CTG GCG TTG CTG CAG TTC CTG GGG GAT GAT GAG Lys Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu 800 805 810 815	2929
ATC GAG ATG CTG GAG CGG CTG TGG CTC TCT GGG ATC TGC CAC AAT GAC Ile Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp 820 825 830	2977
AAA ATC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG GCG GGC Lys Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly 835 840 845	3025
GTC TTC TAC ATG CTC CTG GTG GCC ATG GGC CTG TCC CTG CTG GTC TTC Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe 850 855 860	3073
GCC TGG GAG CAC CTG GTG TAC TGG CCG CTG CCG CAC TGC CTG GGG CCC Ala Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro 865 870 875	3121
ACC CAC CGC ATG GAC TTC CTG CTG GCC TTC TCC AGG GGC ATG TAC AGC Thr His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser 880 885 890 895	3169
TGC TGC AGC GCT GAG GCC GCC CCA CCG CCC GCC AAG CCC CCG CCG CCG Cys Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro 900 905 910	3217
CCA CAG CCC CTG CCC AGC CCC GCG TAC CCC GCG CCG GGG CCG GCT CCC Pro Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro 915 920 925	3265
GGG CCC GCA CCT TTC GTC CCC CCG GAG CCG GCC TCA GTG GCC CGC TGG Gly Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp 930 935 940	3313
CGC CGG CCC AAG GGC GCG GGG CCG CCG GGG GGC GCG GGC CTG GCC GAC Arg Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp 945 950 955	3361
GGC TTC CAC CGC TAC TAC GGC CCC ATC GAG CCG CAG GGC CTA GGC CTC Gly Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu 960 965 970 975	3409
GGC CTG GGC GAA GCG CGC GCG GCA CCG CGG GGC GCA GCC GGG CGC CCG Gly Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro 980 985 990	3457

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CTG TCC CCG CCG GCC GCT CAG CCC CCG CAG AAG CCG CCG GCC TCC TAT	3505
Leu Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr	
995 1000 1005	
TTC GCC ATC GTA CGC GAC AAG GAG CCA GCC GAG CCC CCC GCC GGC GCC	3553
Phe Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala	
1010 1015 1020	
TTC CCC GGC TTC CCG TCC CCG CCC GCG CCC CCC GCC GCC GCG GCC ACC	3601
Phe Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr	
1025 1030 1035	
GCC GTC GGG CCG CCA CTC TGC CGC TTG GCC TTC GAG GAC GAG AGC CCG	3649
Ala Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro	
1040 1045 1050 1055	
CCG GCG CCC GCG CGG TGG CCG CGC TCG GAC CCC GAG AGC CAA CCC CTG	3697
Pro Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu	
1060 1065 1070	
CTG GGG CCA GGC GCG GGC GGC GCG GGG GGC ACG GGG GGC GCA GGC GGA	3745
Leu Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly	
1075 1080 1085	
GGA GCC CCG GCC GCT CCG CCC CCG TGC TTC GCC GCG CCG CCC CCG TGC	3793
Gly Ala Pro Ala Ala Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys	
1090 1095 1100	
TTT TAC CTC GAT GTC GAC CAG TCG CCG TCG GAC TCG GAG GAC TCG GAG	3841
Phe Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu	
1105 1110 1115	
AGC CTG GCC GGC GCG TCC CTG GCC GGC CTG GAT CCC TGG TGG TTC GCC	3889
Ser Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala	
1120 1125 1130 1135	
GAC TTC CCT TAC CCG TAT GCC GAT CGC CTC GGG CSG CCC GCG GCA CGC	3937
Asp Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg	
1140 1145 1150	
TAC GGA TTG GTC GAC AAA CTA GGG GGC TGG CTC GCC GGG AGC TGG GAC	3985
Tyr Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp	
1155 1160 1165	
TAC CTG CCT CCS CGC AGC GGT CGG GCC GCC TGG CAC TGT CGG CAC TGC	4033
Tyr Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys	
1170 1175 1180	
GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC	4081
Ala Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His	
1185 1190 1195	
GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCG CCT CCA CCC TGG GCC	4129
Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala	
1200 1205 1210 1215	
GCC GGG CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG	4177
Ala Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser	
1220 1225 1230	
CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC GCG	4225
His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Ala	
1235 1240 1245	
CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG	4273
Pro His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro	
1250 1255 1260	

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CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT 4321
 Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro
 1265 1270 1275

CGC GCC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC 4369
 Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg
 1280 1285 1290 1295

AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCG CTG CCT ACA GCT TCC 4417
 Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser
 1300 1305 1310

CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG 4465
 His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala
 1315 1320 1325

CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGCGGCC CCGGGGGGCC 4512
 His Phe Ser Ser Leu Glu Ser Glu Val
 1330 1335

CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC 4572

CGCGTGGGTT GGAAGGAAA GCAGTGGAAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG 4632

CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC 4692

AGG 4695

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met
 1 5 10 15

Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala
 20 25 30

Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly Ala
 35 40 45

Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala Ala
 50 55 60

Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser Pro
 65 70 75 80

Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp Pro
 85 90 95

Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg Val
 100 105 110

His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala Pro
 115 120 125

Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser Glu
 130 135 140

His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr
 145 150 155 160
 Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe
 165 170 175
 Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr
 180 185 190
 Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr
 195 200 205
 Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp
 210 215 220
 Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser
 225 230 235 240
 Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val
 245 250 255
 Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp
 260 265 270
 Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Gly Ser Gly Ala Pro
 275 280 285
 Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu
 290 295 300
 Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val
 305 310 315 320
 Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg
 325 330 335
 Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn
 340 345 350
 Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr
 355 360 365
 Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn
 370 375 380
 Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu Val
 385 390 395 400
 Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp
 405 410 415
 Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu
 420 425 430
 Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala
 435 440 445
 Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser
 450 455 460
 Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu
 465 470 475 480
 Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala
 485 490 495

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His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys
 500 505 510
 His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val
 515 520 525
 Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu
 530 535 540
 Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly
 545 550 555 560
 Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala
 565 570 575
 Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met
 580 585 590
 Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser
 595 600 605
 Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly
 610 615 620
 Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val
 625 630 635 640
 Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys
 645 650 655
 Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser
 660 665 670
 Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp
 675 680 685
 Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln
 690 695 700
 Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys
 705 710 715 720
 Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr
 725 730 735
 Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys
 740 745 750
 Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg
 755 760 765
 Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe
 770 775 780
 Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys
 785 790 795 800
 Arg Pro Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Asp Glu Ile
 805 810 815
 Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys
 820 825 830
 Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val
 835 840 845

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Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala
 850 855 860
 Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr
 865 870 875 880
 His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys
 885 890 895
 Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro
 900 905 910
 Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly
 915 920 925
 Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg
 930 935 940
 Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly
 945 950 955 960
 Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly
 965 970 975
 Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu
 980 985 990
 Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe
 995 1000 1005
 Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe
 1010 1015 1020
 Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Thr Ala
 1025 1030 1035 1040
 Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro
 1045 1050 1055
 Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu
 1060 1065 1070
 Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly
 1075 1080 1085
 Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe
 1090 1095 1100
 Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser
 1105 1110 1115 1120
 Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala Asp
 1125 1130 1135
 Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr
 1140 1145 1150
 Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr
 1155 1160 1165
 Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala
 1170 1175 1180
 Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp
 1185 1190 1195 1200

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 1003937 01040E

Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Trp Ala Ala
 1205 1210 1215
 Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser His
 1220 1225 1230
 Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Pro
 1235 1240 1245
 His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro Pro
 1250 1255 1260
 Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro Arg
 1265 1270 1275 1280
 Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg Arg
 1285 1290 1295
 Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser His
 1300 1305 1310
 Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala His
 1315 1320 1325
 Phe Ser Ser Leu Glu Ser Glu Val
 1330 1335

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTCCT ACTCCAAGAT CTGGCCCTAG 60
 TCCATGTTTG C 71

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTGTAG GCAAACATGG 60
 ACTAGGGCCA G 71

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(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGCTACG AAGAGCTCCA CAACCACCTG 60
 G 61

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTGAGACGT CAGACAAAGG AGGCCAGGT GTAGGTGGTC TACCAGGTGG TTGTGGAGCT 60
 CT 62

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGCAGAGCA CCTCCACCAT CTCCTTGTC TACTCCAAGA TCTGGCCCTA GTCCATGTTT 60
 GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACCAC CAGATGGAGG 120
 TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGCC 180
 TCCTTTGTCT GACGT 195

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